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| Phe | Val | Leu | Leu | Ile | Phe | His | Phe | Ser | Arg | Leu | Ala | Val | Thr | Ile | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| Leu | Gln | Ser | Trp | Val | Pro | Pro | Pro | Val | Asp | His | His | Asn | Pro | Pro |
| | | 35 | | | | 40 | | | | | 45 | | | |

| Phe | Pro | Asp | Gln | Asn | Leu | Lys | Asp | Pro | Thr | Glu | Asn | Asp | Asn | Ser | Ala |
| | 50 | | | | 55 | | | | | 60 | | | | | |

| Thr | Gly | Ser | Gly | Ala | Pro | Pro | Pro | Ala | Leu | Val | Glu | Pro | Glu | Glu | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

| Gln | Arg | Pro | Pro | Leu | Thr | Thr | Asp | Ser | Asp | Asp | Ser | Pro | Thr | Pro | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |

| Lys | Glu | Arg | Leu | Asp | Thr | Pro | Ser | Asn | Val | Pro | Ser | Gln | Glu | Pro | Glu |
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| Phe | Asp | Ala | Ala | Arg | Leu | Gln | Thr | Gly | Ala | Gln | Thr | Gln | Asn | Lys | His |
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| Glu | Asp | Asp | Glu | Asp | Ile | Val | Pro | Ile | Ser | His | Trp | Lys | Pro | Met | Pro |
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| Glu | Arg | His | Pro | Val | Ser | Pro | Glu | Ala | Leu | Ile | Lys | Leu | Pro | Thr | Gly |
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| Gln | Ser | Lys | Glu | Leu | Pro | Gln | Leu | Gln | Ala | Lys | Phe | Lys | Asp | Glu | Ser |
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| Ser | Ser | Asp | Lys | Met | Gln | Arg | Leu | Gln | Gln | Leu | Asp | Thr | Ile | Lys | Ser |
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| Trp | Gly | Ala | Thr | Leu | Val | Asp | Ala | Leu | Asp | Thr | Leu | Trp | Ile | Met | Asp |

5

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Arg Thr Leu Gly Gly Met Leu Gly Ala Thr Asp Ile Ser Gly His Lys
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Thr Asp Ile Leu Leu Glu Lys Ser Val Glu Leu Ala Asp Val Leu Met
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Leu Ala Glu Leu Gly Ser Leu Ser Leu Glu Phe Thr Arg Leu Ala Gln
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Asn Ser Thr Ser Ser Val Ser Thr Arg Thr Arg Gln Ile His Glu Gly
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6

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8

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<210>   6
<211>   505
<212>   PRT
<213>   Aspergillus nidulans

<400>   6
Met Arg Thr Leu Leu Ala Leu Ala Ala Phe Ala Gly Phe Ala Ala Ala
1               5                   10                  15


Arg Val Pro Ala Thr Ala Ile Thr Arg Pro Val Met Arg Ser Asp Ser
                20                  25                  30
```

10

```
Arg Ala Asp Ala Val Lys Glu Ala Phe Ser His Ala Trp Asp Gly Thr
        35              40              45

Thr Asn Thr Ala Phe Pro His Asp Glu Leu His Pro Ile Ser Asn Gly
    50              55              60

Thr Gly Asp Ser Arg Asn His Trp Gly Ala Ser Ala Val Asp Ala Leu
65              70              75              80

Ser Thr Ala Ile Met Met Arg Asn Ala Thr Ile Val Asn Gln Ile Leu
                85              90              95

Asp His Ile Ala Ala Val Asp Thr Ser Lys Thr Asn Ala Met Val Ser
            100             105             110

Leu Phe Glu Thr Thr Ile Arg Thr Leu Ala Gly Met Ile Ser Gly Thr
        115             120             125

Asp Leu Leu Lys Gly Pro Ala Ala Gly Leu Val Asp Asp Ser Arg Val
    130             135             140

Asp Val Leu Leu Glu Gln Ser Gln Asn Leu Ala Glu Val Leu Lys Phe
145             150             155             160

Ala Phe Asp Thr Pro Ser Gly Val Pro Thr Asn Met Ile Asn Ile Thr
            165             170             175

Ser Gly Gly Asn Asp Gly Ala Thr Thr Asn Gly Leu Ala Val Thr Gly
            180             185             190

Thr Leu Val Leu Glu Trp Thr Arg Leu Ser Asp Leu Thr Gly Asn Asp
    195             200             205

Glu Thr Ala Arg Leu Ser Gln Arg Ala Glu Asp Thr Leu Leu His Pro
    210             215             220

Glu Pro Ala Gln Thr Glu Pro Phe Pro Gly Leu Ile Gly Ser Ala Val
225             230             235             240

Asn Ile Ala Asp Gly Lys Leu Ala Asn Gly His Ile Ser Trp Asn Gly
            245             250             255

Gly Ala Asp Ser Thr Thr Glu Thr Leu Ile Lys Met Thr Val Thr Asp
            260             265             270
```

11

```
Pro Glu Arg Phe Gly Leu Thr Arg Asp Arg Trp Val Ala Ala Ala Glu
        275             280             285

Ser Ser Ile Asn His Leu Ala Ser His Pro Ser Thr Arg Pro Asp Val
        290             295             300

Thr Phe Leu Ala Thr Thr Asn Glu Glu His Gln Leu Gly Leu Thr Ser
305             310             315             320

Gln His Leu Thr Cys Phe Asp Gly Gly Ser Phe Leu Leu Gly Gly Thr
                325             330             335

Leu Leu Asp Arg Gln Asp Phe Val Asp Phe Gly Leu Asp Leu Val Ala
            340             345             350

Gly Cys His Glu Thr Thr Asn Ser Thr Leu Thr Gly Ile Gly Pro Glu
        355             360             365

Gln Phe Ser Trp Asp Pro Asn Gly Val Pro Asp Ser Gln Lys Glu Leu
    370             375             380

Phe Glu Arg Ala Gly Phe Thr Ile Asn Ser Gly Gln Thr Ile Leu Arg
385             390             395             400

Pro Glu Val Ile Glu Ser Phe Thr Thr Ala Trp Arg Val Thr Gly Asp
            405             410             415

Gly Thr Thr Leu Glu Trp Val Trp Asn Ala Phe Thr Asn Ile Asn Lys
            420             425             430

Thr Cys Arg Thr Ala Thr Gly Phe Ala Gly Leu Glu Asn Val Asn Ala
        435             440             445

Ala Asn Gly Gly Gly Arg Ile Asp Asn Gln Glu Ser Phe Met Phe Ala
    450             455             460

Glu Val Leu Lys Thr Ser Phe Leu Thr Phe Ala Pro Glu Asp Asp Trp
465             470             475             480

Gln Val Gln Lys Gly Ser Gly Asn Thr Phe Val Thr Asn Thr Glu Ala
            485             490             495

His Pro Phe Lys Val Thr Thr Pro Gln
            500             505
```

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<210>    7
<211>    6
<212>    DNA
<213>    Aspergillus nidulans

<400>    7
gtaagt                                                                    6


<210>    8
<211>    6
<212>    DNA
<213>    Aspergillus nidulans

<220>
<221>    variation
<222>    (4)..(4)
<223>    N = A, C, G, or T

<400>    8
gtangt                                                                    6


<210>    9
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<212>    DNA
<213>    Aspergillus nidulans

<400>    9
gctgac                                                                    6


<210>    10
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<212>    DNA
<213>    Aspergillus nidulans

<400>    10
rctrac                                                                    6


<210>    11
<211>    6
<212>    DNA
<213>    Aspergillus nidulans

<400>    11
gtacgt                                                                    6


<210>    12
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<212>    DNA
<213>    Aspergillus nidulans

<400>    12
actgac                                                                    6
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<210> 13
<211> 10
<212> PRT
<213> Asperfillus nidulans

<400> 13
Gly Gly Leu Gly Glu Ser Phe Thr Glu Thr
1   5   10

<210> 14
<211> 9
<212> PRT
<213> Aspergillus nidulans

<400> 14
Leu Ala Glu Thr Leu Lys Thr Leu Thr
1   5

<210> 15
<211> 29
<212> DNA
<213> PCR Primer

<220>
<221> y represents c, t, or u; r represents g or a; n represents a, c, g, t, or
u; and h represents a, c, t, or u
<222> (1)..(29)
<223>

<400> 15
ggyggyctng gygartcntt ctacgagta   29

<210> 16
<211> 33
<212> DNA
<213> PCR Primer

<220>
<221> y represents c, t, or u; r represents g or a; n represents a, c, g, t, or
u; and h represents a, c, t, or u
<222> (1)..(33)
<223>

<400> 16
gtanaggtac ttnagngtct cngcnagrha gaa   33

<210> 17
<211> 2032
<212> DNA
<213> Aspergillus nidulans

<400> 17
atcgatgtct gctgcataaa ggcagacgga ggaagatgcc gagacggtgg tcctccctca   60

tcagcatcac agccatcttc ttggtcctct tcttcctcct tcataggaat acagacacac   120

```
cacgcgccgc caatagggct acaaacggcc ctgccaacgg ctttgctagg cagcaaagca   180

tatgtccatc aacacccct cagcctccat ataaccgaac cagcacggga gggttcaact   240

ggggtgaaat cccagtcaga taccctgtat ccgacttcat cccgctgtca accaactctc   300

ctgcaacact tccgcgcatc caacgctctt ccttcccact tcaatcctca atcactaaat   360

cccgccaggc agcagtcaaa ggtgcctttc agcgcgcatg gacctcctac acaacccacg   420

cctggaaggc ggacgaggta cggcccatca cggccggatc tcgaaacaac tttggcggat   480

ggggagcgac cctagtcgac aatctcgaca cactgctaat catggggctg gacgaggagt   540

tcgcagcggc agtcgacgcg ctcgcagata tagaattcag cccgcactcg tccccatcct   600

cctcccagag cacaatcaac atattcgaaa cgacaatccg gtatctgggc ggcttgctcg   660

cggcgtatga tctcactggc tgtcgagaga ctcggctgct ggacaaagca atccagcttg   720

gggagatgat ctacacctcc ttcgacacag agaaccgcat gcccgtacca cggtggaatc   780

tgcacaaagc aggcaacgga gagcctcagc gcgcggcagt gcagggcgtg ctcgctgaac   840

tcgccagcag cagtctcgag ttcacgcggc tgtcgcagct gacgggggat atgcggtatt   900

tcgatgcggc atcccgcatt accgatctgc ttgactccca agccggccat acccggatcc   960

cggggttgtg gccagtcagc gtgaacctgc agaaaggcga tctgacccgt gggtcgacat   1020

tcagttttgg cgggatggcc gatagcgcct acgagtatct cggcaagacg tatcggctcc   1080

tcggtggtgt ggggaaaggg ccacagtacg agcgtctggc gcgaaacgca ctagatgccg   1140

ggattcgaca tctcctcttc cgaccgatga cgcctgatca tgcagatatc ctcctacccg   1200

gggtcgcgca cgcaaccagc tcttccgtgg gactcgagcc ccggacagag catctcgcct   1260

gttttgtggg tgggatgtac gcgctcgccg ggaagctttt ctcaaaccag acgtacctcg   1320

acaccggccg gaagctgaca gacggttgta tctggtacta cgataattca ccgctaggta   1380

tcatgccgga gatgttcacc gtgccggctt gtccgtcagt ggctgaatgt ccttgggacg   1440

aaacaagggg tggtatctac acctacgtgc gtgatgggca ctactttctg cgtcctgagg   1500

caatggagag tatcttctat atgtggcgca ttacagggga cgaaaagtac cgcgaggctg   1560

catggagaat gttcacggct atcgaagcgg ttacaaagac ggagtttggg aatgcggcgg   1620

tgcgggatgt tatggttgag gaaggaaatg taaagagaga agatagcatg gagagtttct   1680

ggatggcaga gacgttgaag tatctgtatc tgatatttgg ggagaccgat ttggtcagct   1740

tggacgactg ggtgttcaat acggaggcgc acccttttgag gggtgcaggg agttgacatt   1800

gtattcacac atcggtatag acaaattata gagtagacgt tcaaaacggc caaaactgaa   1860

tggatagact ccatatgcat tgaatataca atgtattcgc tgcaaagcat ggataaaata   1920
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15

aagatgtaca aagtgtcttt gttgtcgctt tgaaagtggt atatcatccc atcataaggt   1980

ggcagtgtaa ccaaccctct atatcaccta catagacagc tgatagaccg gc   2032

<210> 18
<211> 586
<212> PRT
<213> Aspergillus nidulans

<400> 18
Met Pro Arg Arg Trp Ser Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu

1   5   10   15

Val Leu Phe Phe Leu Leu His Arg Asn Thr Asp Thr Pro Arg Ala Ala
          20   25   30

Asn Arg Ala Thr Asn Gly Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser
          35   40   45

Ile Cys Pro Ser Thr Pro Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr
     50   55   60

Gly Gly Phe Asn Trp Gly Glu Ile Pro Val Arg Tyr Pro Val Ser Asp
65   70   75   80

Phe Ile Pro Leu Ser Thr Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln
               85   90   95

Arg Ser Ser Phe Pro Leu Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala
          100   105   110

Ala Val Lys Gly Ala Phe Gln Arg Ala Trp Tyr Ser Thr Thr Thr His
          115   120   125

Ala Trp Lys Ala Asp Glu Val Arg Pro Ile Thr Ala Gly Ser Arg Asn
     130   135   140

Asn Phe Gly Gly Trp Gly Ala Thr Leu Val Asp Asn Leu Asp Thr Leu
145   150   155   160

Leu Ile Met Gly Leu Asp Glu Glu Phe Ala Ala Ala Val Asp Ala Leu
               165   170   175

Ala Asp Ile Glu Phe Ser Pro His Ser Ser Pro Ser Ser Ser Gln Ser
          180   185   190

16

```
Thr Ile Asn Ile Phe Glu Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu
        195             200             205

Ala Ala Tyr Asp Leu Thr Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys
        210             215             220

Ala Ile Gln Leu Gly Glu Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn
225             230             235                     240

Arg Met Pro Val Pro Arg Trp Asn Leu His Lys Ala Gly Asn Gly Glu
                245             250             255

Pro Gln Arg Ala Ala Val Gln Gly Val Leu Ala Glu Leu Ala Ser Ser
            260             265             270

Ser Leu Glu Phe Thr Arg Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr
        275             280             285

Phe Asp Ala Ala Ser Arg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly
        290             295             300

His Thr Arg Ile Pro Gly Leu Trp Pro Val Ser Val Asn Leu Gln Lys
305             310             315                     320

Gly Asp Leu Thr Arg Gly Ser Thr Phe Ser Phe Gly Gly Met Ala Asp
                325             330             335

Ser Ala Tyr Glu Tyr Leu Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val
            340             345             350

Gly Lys Gly Pro Gln Tyr Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala
            355             360             365

Gly Ile Arg His Leu Leu Phe Arg Pro Met Thr Pro Asp His Ala Asp
        370             375             380

Ile Leu Leu Pro Gly Val Ala His Ala Thr Ser Ser Ser Val Gly Leu
385             390             395                     400

Glu Pro Arg Thr Glu His Leu Ala Cys Phe Val Gly Gly Met Tyr Ala
            405             410             415

Leu Ala Gly Lys Leu Phe Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg
            420             425             430
```

```
Lys Leu Thr Asp Gly Cys Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly
        435             440             445

Ile Met Pro Glu Met Phe Thr Val Pro Ala Cys Pro Ser Val Ala Glu
        450             455             460

Cys Pro Trp Asp Glu Thr Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp
465                 470             475                 480

Gly His Tyr Phe Leu Arg Pro Glu Ala Met Glu Ser Ile Phe Tyr Met
            485             490                 495

Trp Arg Ile Thr Gly Asp Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met
            500             505                 510

Phe Thr Ala Ile Glu Ala Val Thr Lys Thr Glu Phe Gly Asn Ala Ala
        515             520                 525

Val Arg Asp Val Met Val Glu Glu Gly Asn Val Lys Arg Glu Asp Ser
    530             535                 540

Met Glu Ser Phe Trp Met Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile
545                 550             555                 560

Phe Gly Glu Thr Asp Leu Val Ser Leu Asp Asp Trp Val Phe Asn Thr
            565             570                 575

Glu Ala His Pro Leu Arg Gly Ala Gly Ser
            580             585


<210>   19
<211>   6
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Consensus Splice Site

<220>
<221>   variation
<222>   (1)..(1)
<223>   R = G or A

<220>
<221>   variation
<222>   (4)..(4)
<223>   R = G or A

<400>   19
rctrac                                                          6
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